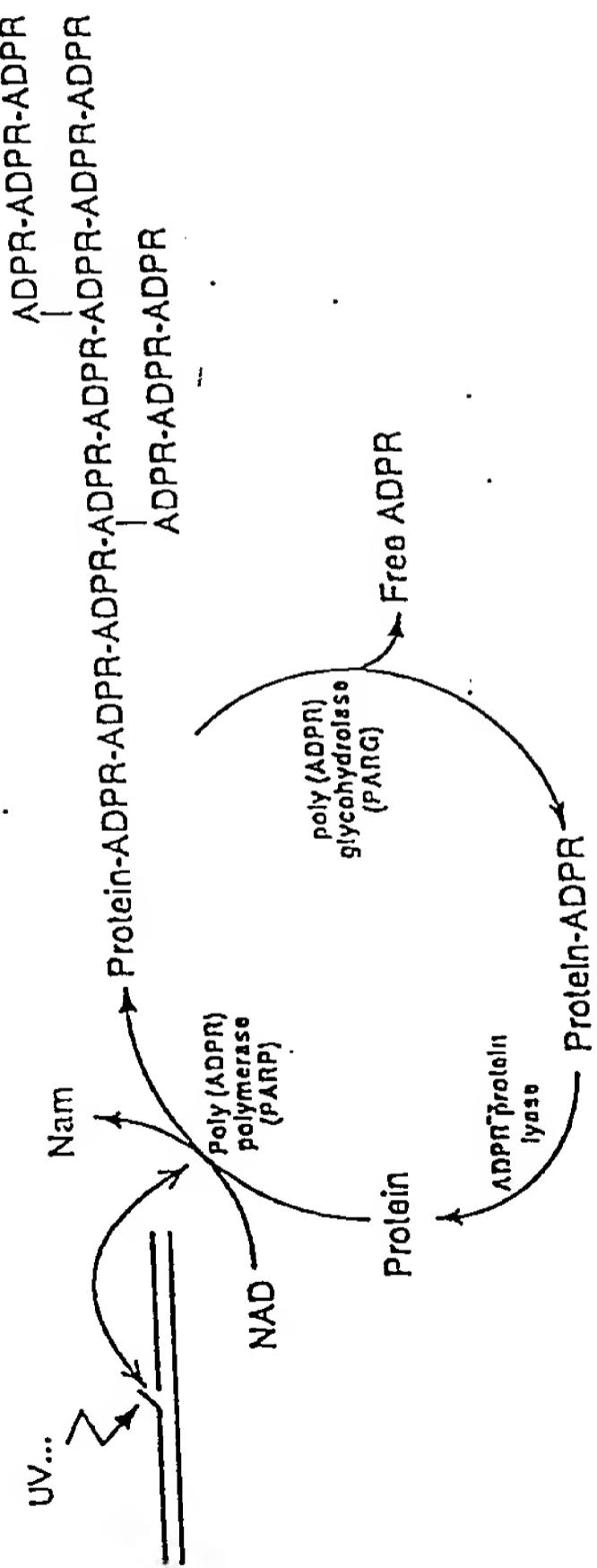
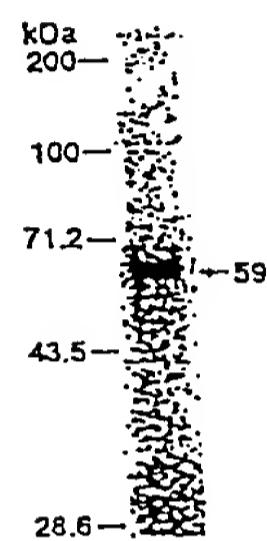


FIGURE 1



## FIGURE 2



# FIGURE 3

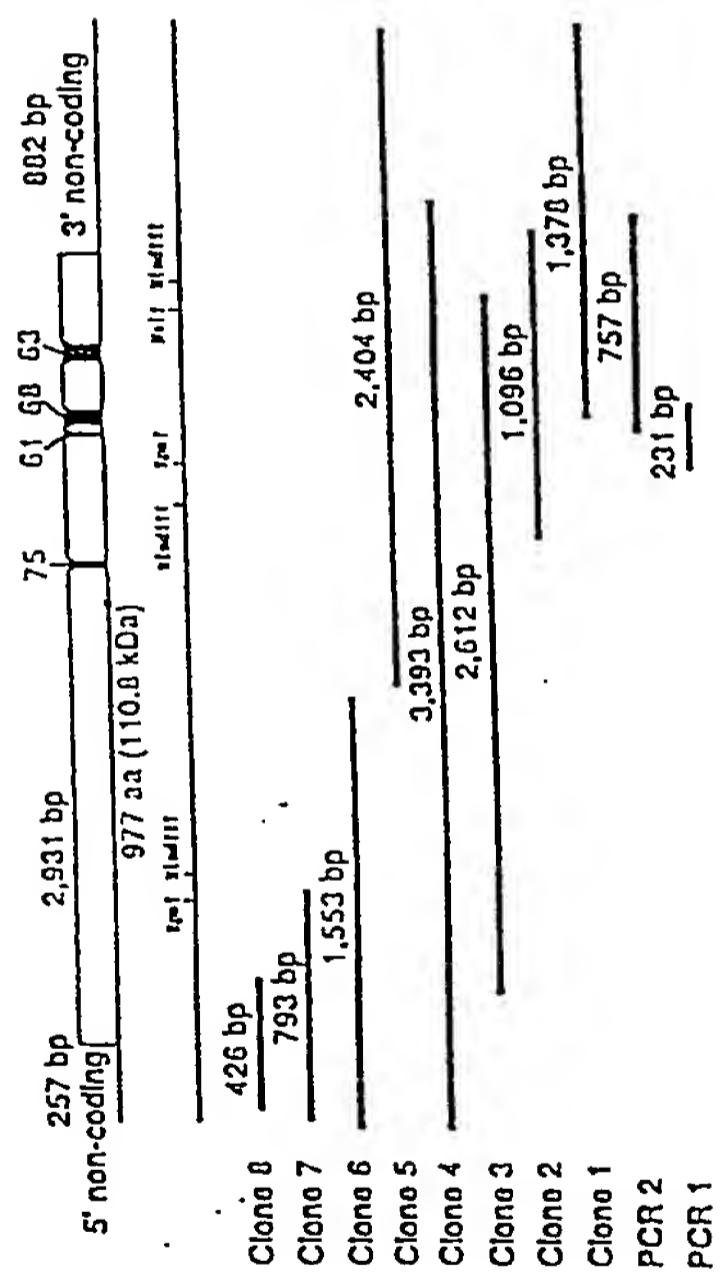
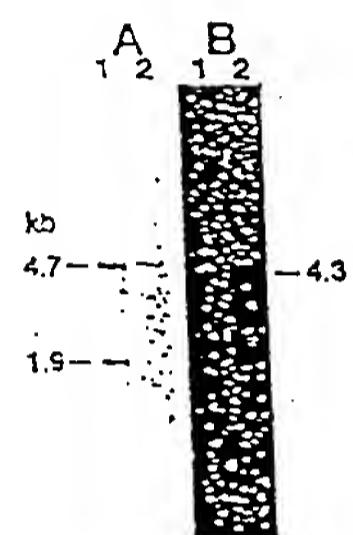


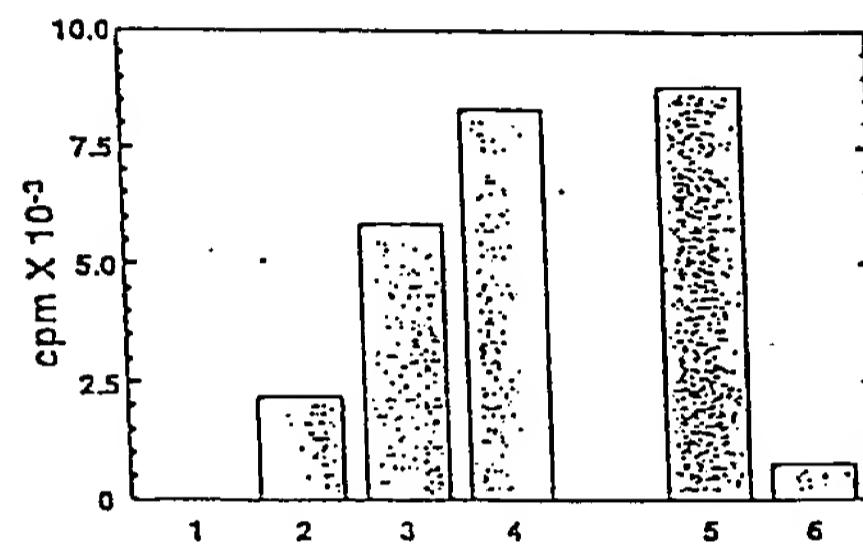
FIGURE 4



## FIGURE 5

bPARG	(422)	ED. . . . . KRIKEQCEEMKHQRTE. . . RKİPKYI PPH	SEQ ID NO: 19
hPARG	(421)	ED. . . . . RRKEQWETKHZQRTE. . . RKİPKYVPPH	SEQ ID NO: 20
mPARG	(413)	ED. . . . . RRKEQCEVRHQRTE. . . RKİPKYI PPN	SEQ ID NO: 21
CePARG	(29)	HQVPTMKRKLTEHGNNTESLILKEDPEEPEPKS	SEQ ID NO: 22
hPARP	(205)	EG. . . . . KRKG D. EVDG. VDEVAKKKSKKEKDK	SEQ ID NO: 23
mPARP	(205)	EG. . . . . KRKG D. EVDG. TDEVAKKKSRKETDK	SEQ ID NO: 24
bPARP	(208)	EG. . . . . KRKG D. EVDG. IDEVTKKKKSKKEKDK	SEQ ID NO: 25
aPARP	(205)	EG. . . . . KRKG E. EVDG. . MIVVAKKKSRKEKEK	SEQ ID NO: 26
XIPARP	(204)	EG. . . . . KRKG D. EVDG. HSAATKKKLIKKEKEK	SEQ ID NO: 27
DmPARP	(202)	EELPDTKRAKM. ELSDTNNEEGEKKQQR. . . . .	SEQ ID NO: 28
SpPARP	(205)	EGVSSAKKAKT. EKIDEEADAASIKELTEKIKK	SEQ ID NO: 29

# FIGURE 6



# FIGURE 7

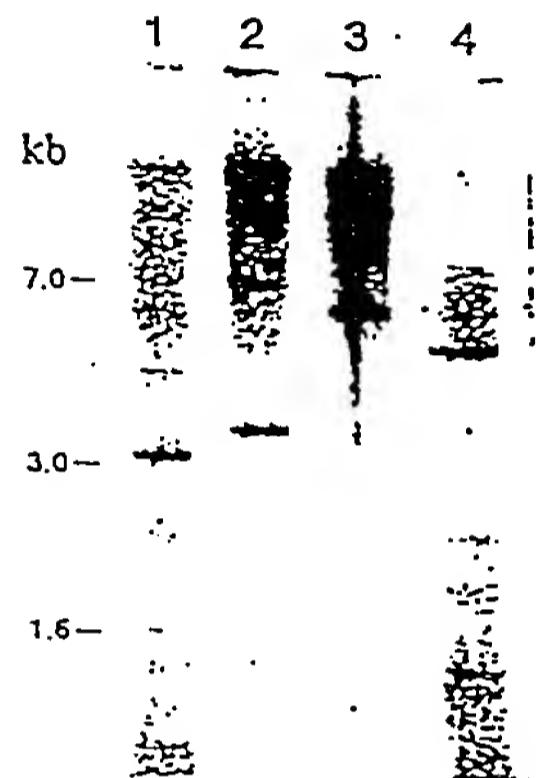


FIGURE 8

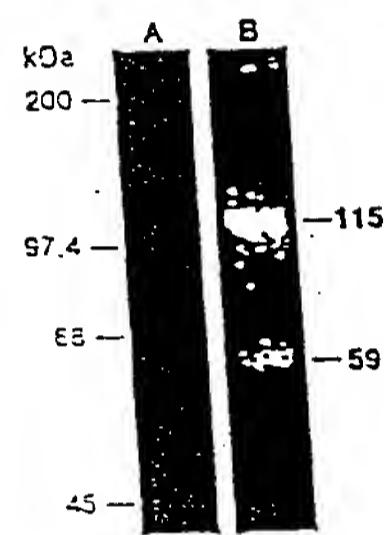
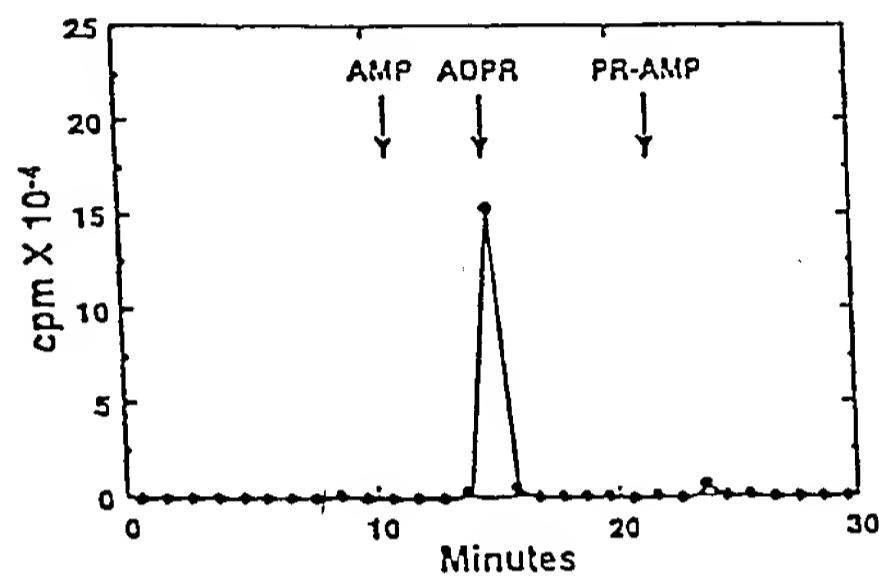
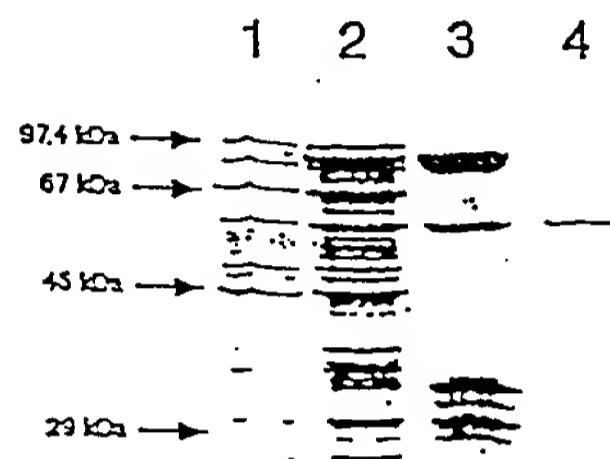


FIGURE 9



# FIGURE 10



## FIGURE 11

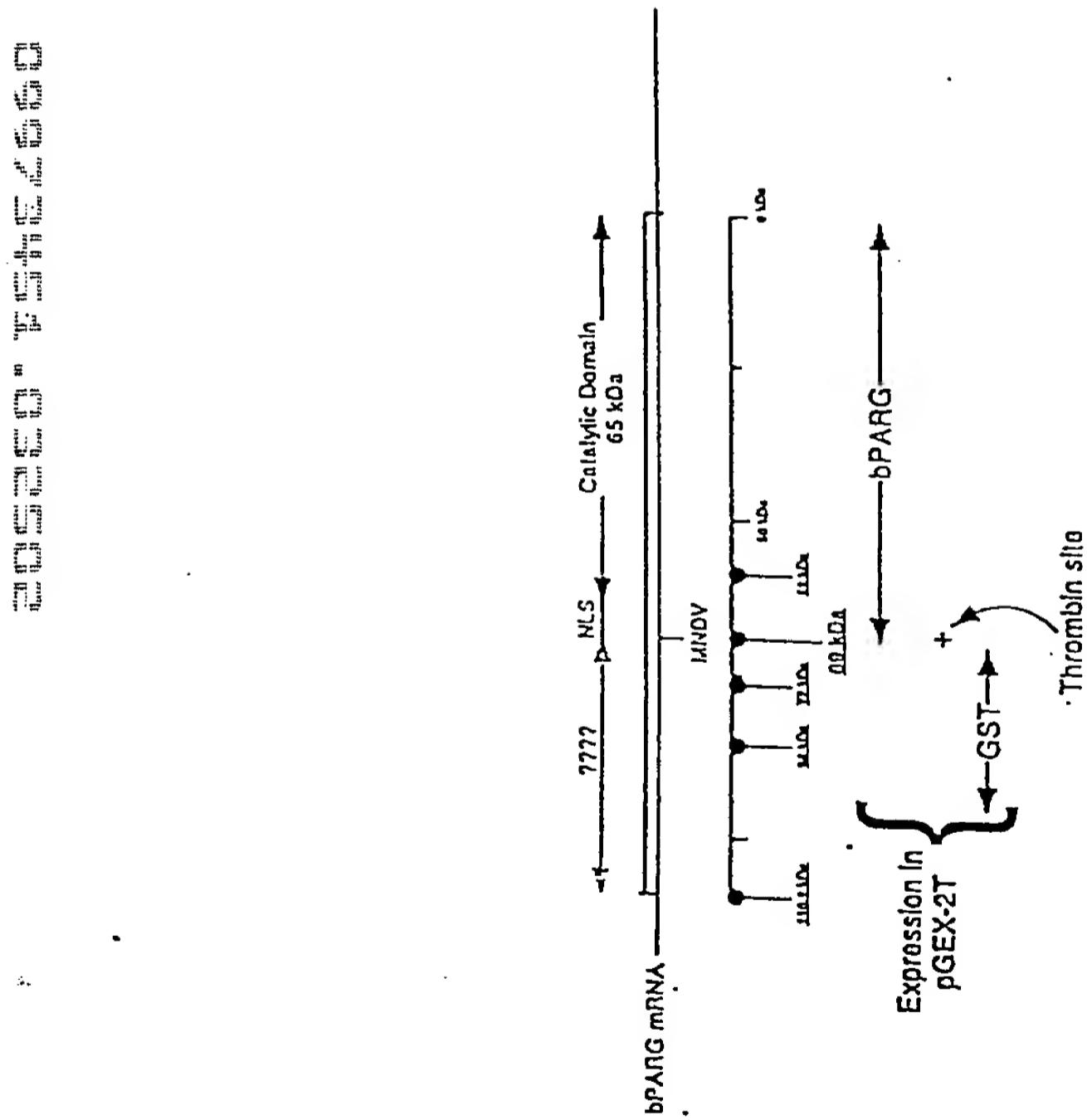


FIGURE 12

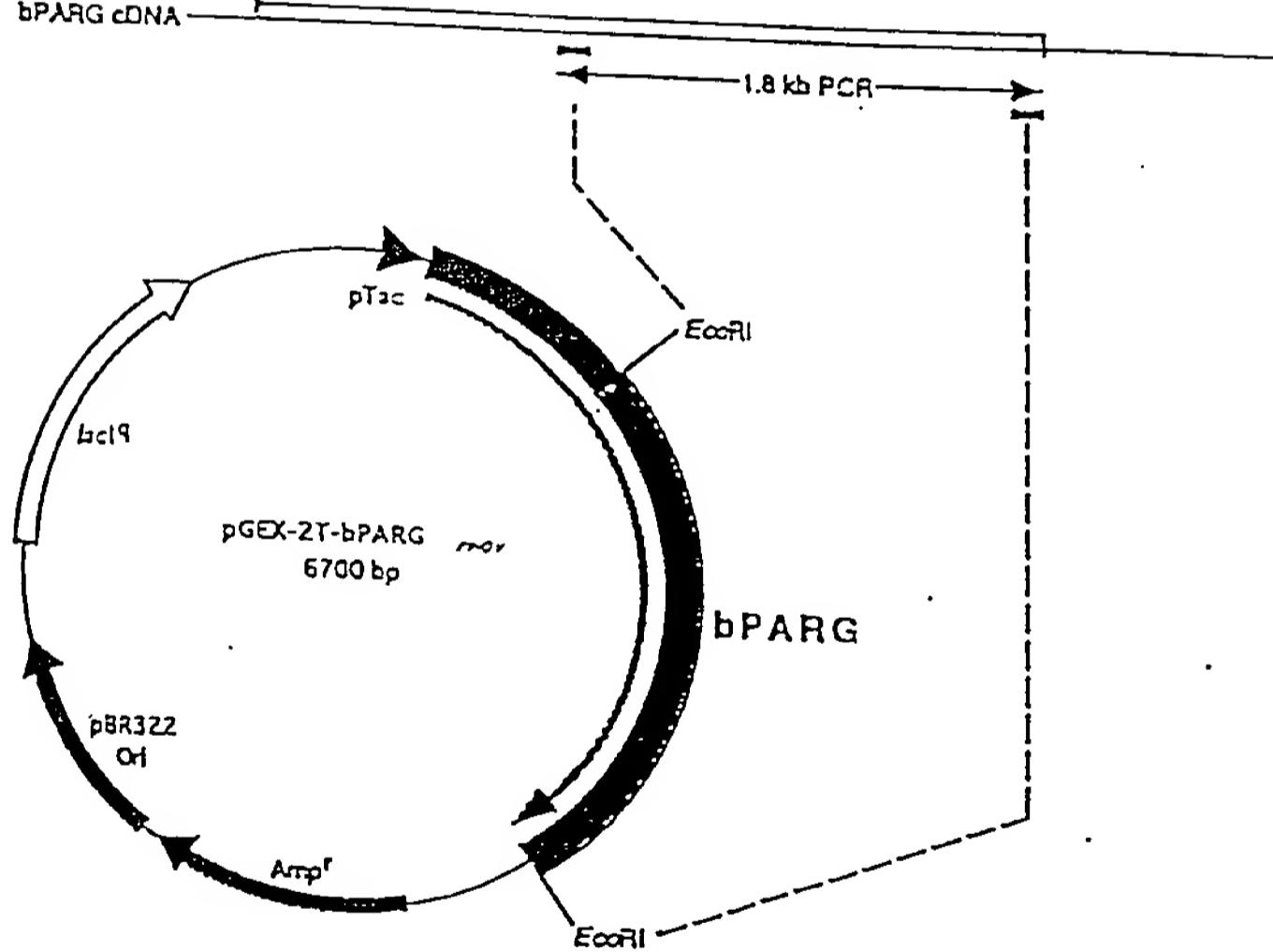


FIGURE 13

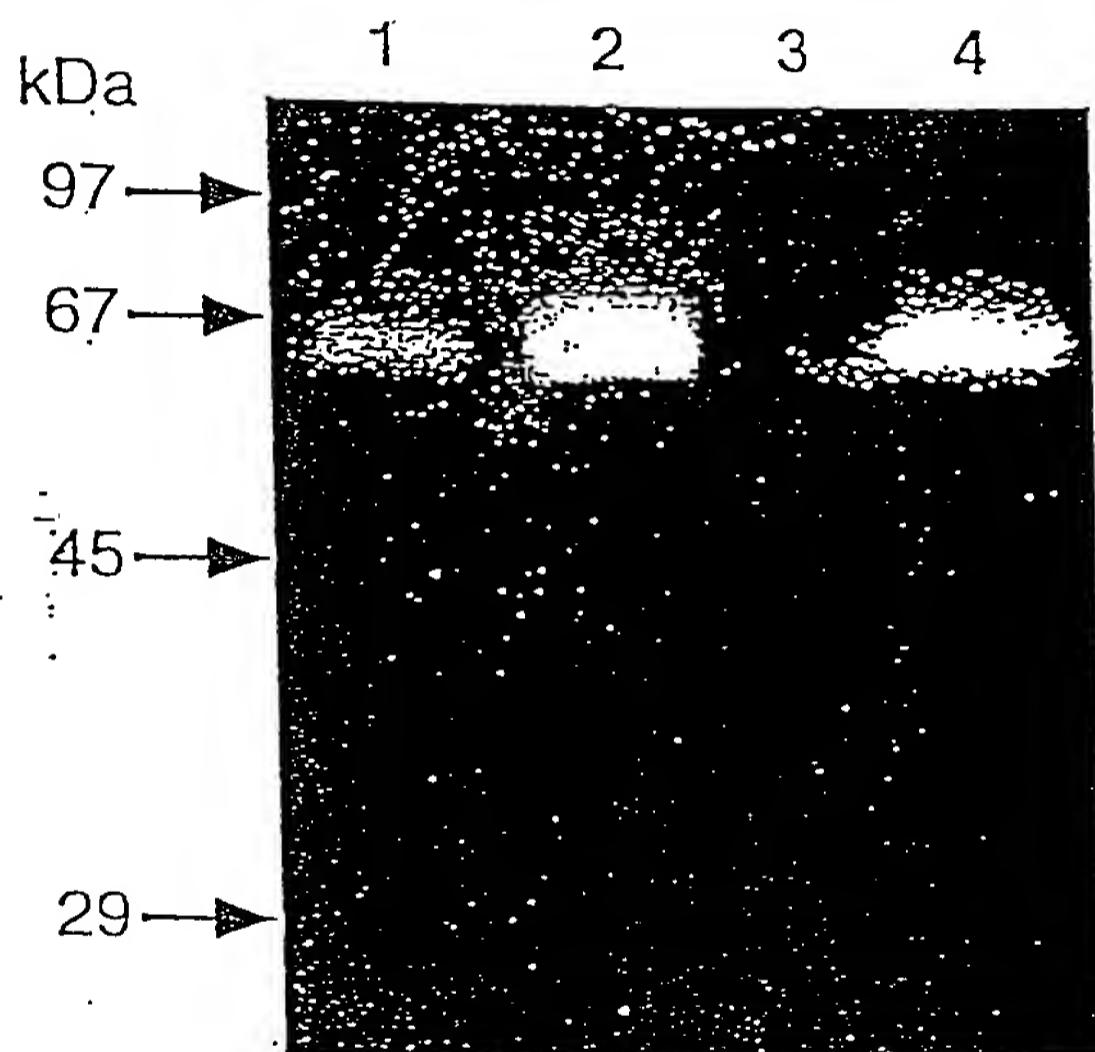
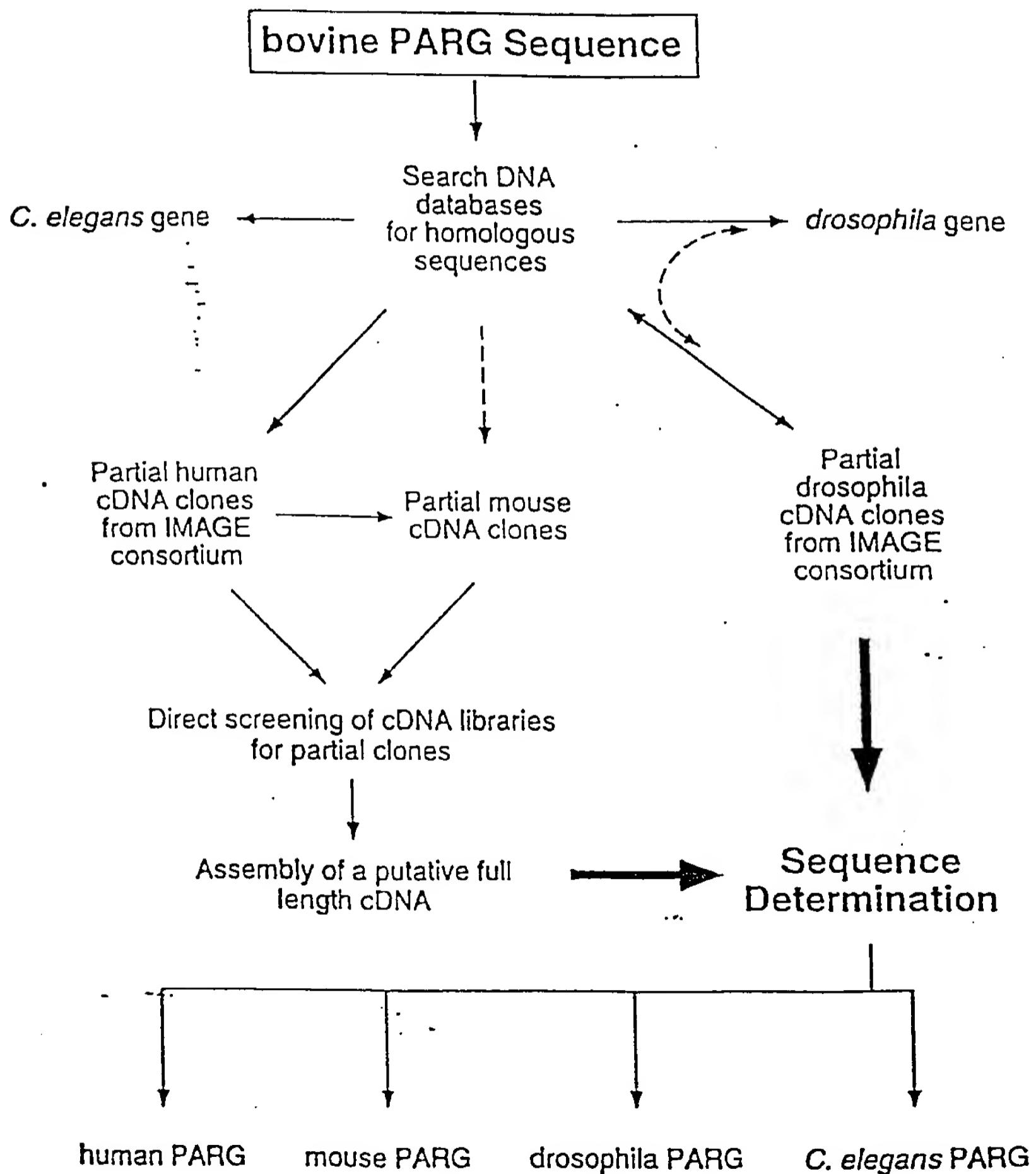


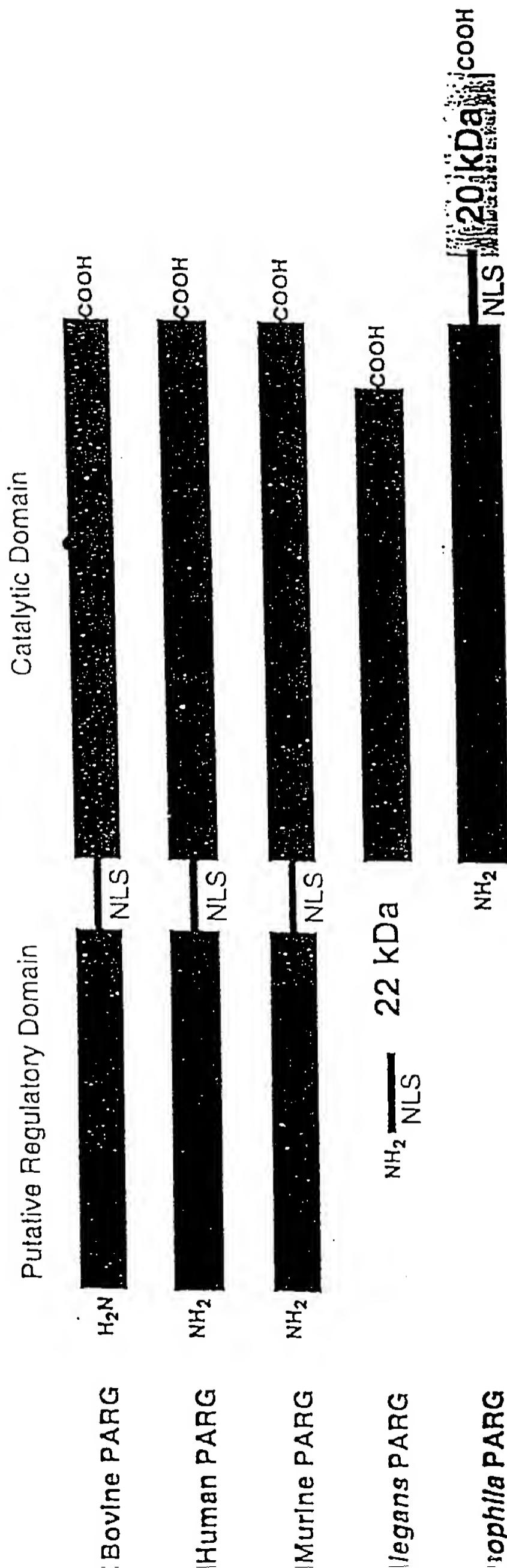
FIGURE 14

## Strategy to Obtain Homologous PARG Sequences



# Domain Organization of PARGs

FIGURE 15



# FIGURE 16

## Multiple Alignment of Amino Acid Sequences of PARG from Different Species

Bparg 1 MSAGPGCEPCTKRPRWDAATSPPAASDAREFFCRQRRVLDSDKDAPVQFRVPPSSSGCALGRAGQERGSATSLVFKQKTTITSMMDTKGIKTVESESLSK  
 Bparg 1 MHAGPGCEPCTKATRWGARTTS..PARSDARSPFSRQRRVLDPKDAHVQFRVPPSSPACVPGQAGQERGSATSLVFKQKTTITSMMDTKGIKTAKSESLSK  
 Mparg 1 MSAGPGHEPCTKA..RWGARGTSAPTAEDSRSPFPCRQRRVLDPKDAPVQFRVPPSSPACVSGRAGPERGATSIVFKQKTTITSMMDTKGPKTAEE..SK  
 Dparg 1 -----  
 Ceparg 1 -----

Bparg 101 EHHETREESSHHSSVQKDEPIQRRMEEKLEEVSQLGFDKSPVVKGTQILKQHQTAAXCKNQNEGPHSERLLESEPPAVTLVPEQFSWANVDOSSPKDDDESDT  
 Bparg 100 EHHETRIEKSMMSSVQKDEPIQRRMEEKLEEVSQLSLDKSLTEKSTQILKQHQTAAXCKNQNEGKETRQLLESEPPQTVTLVPEQFSWANIDRSPQHDDDESDT  
 Mparg 97 EHHETRIDSSMMSSVQKDEPIPKVKLEEVSQLNLDKSPTEKSSQILKQHQTAASVCKNQNEGKETRQLLESEPPAGTPLPKQLEWANIGQSPETDDDESDT  
 Dparg 1 -----  
 Ceparg 1 -----MSKRFIGELGDPVTQDEKDIEDI

Bparg 201 MSEE5RDHQOFLTEVKL...AAAKQTMEDEQGREAERSHQKCGKACEPAAACAGCQQETDVVSESPLSDTGSEDVGTGLKHNARLWRQESSLGNSPPFEK  
 Bparg 200 DSEEHRDQHQFLTTVKL...AAAKQTTEDEHAREAK5EQKCSKSCHPGEDCASCQQETDVVSPKSPLSDVGSSEDVGTGSKNDHKLTRQESCLGNSPPFEK  
 Mparg 197 DHEEDRDEHQHQFLTPIKL...AAKPTIVGDQ...ARSNCKCSCSRQSVKDCTGCQQEVDVLPKSPLSDVGAEDIGTGPKNDHKLTCQESSLGNSPPFEK  
 Dparg 1 -----  
 Ceparg 23 VGVGFAHQVPTMKRRELTERGHTTESKEDPEEPKSRDVFVSSQSSDESQEDSAEAEPEIAKEVSENCENLTETLKISHIESLDHVTERSEHTLD...EK

Bparg 298 ESEPESPMDVDSKWSQCDSEADEETSPGPDE.QEDSSSAQTAHKPSRFQPREADTELKRS SAKGGEIRLHFQFEGGESRAGHN..DWAHKPGSTSSLM  
 Bparg 297 ESEPESPMDVDSKESKSCQDSEADEETSPGPDE.QEDGESSQTAHKPSRFQARDADIEPRKRYSTKGGEVRLHFQFEGGESRTGHN..DWAHKPGHISSLM  
 Mparg 291 ESEPESPMDVDSKESKSCQDSEADEETSPVYDE.QDDRSS..QTAHKLSSCQAREADGDLKRYLTKGSEVRLHFQFE..GENHAGTS..DWAHKPGHSSSLM  
 Dparg 1 -----HQKFRSHLIPPIFQ..KVIQTS..TAHRR..ASAEVL.  
 Ceparg 119 STEPHEE..DVNNKSMIDVAINSDEDDELVLEENHKEHRDGEQVQQLS..QDLFADDQELIEIPGIMHKDITQLDITSEVETAQKMEMIEETADSTFVG

Bparg 396 VECRNSKQHGRKDSSITDEPHRVPKAEDKRKEQCEMKHQRTTERKIPKIIIPPLSPDKEWLGTPIEEM..RRMPRCGIRLPPPLRPSAHTVTVIRVDLLRIG  
 Bparg 395 VECRNSKQHGRKDSSITDEHLRVPKAEDRRKEQWETKEQRTTERKIPKIVPPPLSPDKEWLGTPIEEM..RRMPRCGIRLPPPLRPSAHTVTVIRVDLLRAG  
 Mparg 387 VECRSSSKQHGRKDSSITDEPHRISKSZDRKEQCEVREQRTTERKIPKIIIPPLSPDKEWLGTPIEEM..RKPMPRCGIELPSSLRPSAHTVTVIRVDLLRAG  
 Dparg 32 ....TNRLOK...ALCLCARMSSKSPDGGISIEK....TREZ..PEWLAWSL..DDSNRGVSHEAIEHNRQPFELENLPPVTAGELERVYQLFIRET.  
 Ceparg 216 EDSKATKTVRTSSSF..LSTVSTCRAFAKGRARMIQKELEKHEVIAFTEGNLT....LQPDLNKVDPDRNTRI..CTIPNFFPASQG...KLRED..WRYC

Bparg 494 EKPK..PPPTHEFKDLWDNKEVKMPCSEQNLVPEDENGE..RAAGSRMELIQTALLERLTPQNLKDAILKYNVAYSKKWDFTALIDFWDKVLEEAQELY  
 Bparg 493 EKPK..PPPTHEFKDLWDKKEVKMPCSEQNLVPEDENGE..RTAGSRMELIQTALLERLTPQNLKDAILKYNVAYSKKWDFTALIDFWDKVLEEAQELY  
 Mparg 485 EKPK..PPPTHEFKDLWDKKEVKMPCSEQNLVPEDENGE..RTAGSRMELIQTALLERLTPQNLKDAILKYNVAYSKKWDFTALIDFWDKVLEEAQELY  
 Dparg 115 .PPR..PKKSPGK..WDSEZVRLPCAPESKIPRENPDGS..TIDFRMHEMIEKALLQPIKTCEELQAAIISYNTTDRQWEFRALHQLDEESETRVFF  
 Ceparg 303 ..PKIVLPQRHRE..FDSRGRR...RDSIYIFKRLDGTLKCITTTGTFMFVGLLH.....HMM..FDPDITK...LPAL..EHIYKEMSKLVGREEV

Bparg 592 QSIILPDHVVKIALCLPMICTQPIPLLKQKMHHSITHS5QEQIASLLAAFFCTFPRRHA..KMKSEIISYIPDIMPFLFEGRS5RKPEKLKTLFCYFRRV..T  
 Bparg 591 QSIILPDHVVKIALCLPMICTQPIPLLKQKMHHSITHS5QEQIASLLAAFFCTFPRRHA..KMKSEIISYIPDIMPFLFEGRS5RKPEKLKTLFCYFRRV..T  
 Mparg 583 QSIILPDHVVKIALCLPMICTQPIPLLKQKMHHSVTHS5QEQIASLLAAFFCTFPRRHA..KMKSEIISYIPDIMPFLFEGRS5RKPEKLKTLFCYFRRV..T  
 Dparg 210 EDLLPRIIRLALRLPDLIQSPVPLKKEKMASL8SQQKESCLLAAFLCTFPRRNTLKRKSEIYSTFPDINFHRLIQTGPAVLEKLKCIHETFRRVCPT  
 Ceparg 384 LEKFARVARIAKTAEDILPERITRLVGOVE..SATLS8KQCAALVARMFYF.....RPDSFYS.....FCRILSSDKSICVERLKFLFTYF.....

Bparg 689 EKK....PTGLVTFIRQS..L..ED..F..PEWERCEKLL..TRLEVTTIEGNGQGMLOQDFANRFPVGGCVTSAGLVQEEIRFLINPELIVSRLFTEVLDH  
 Bparg 688 EKK....PTGLVTFIRQS..L..ED..F..PEWERCEKPL..TRLEVTTIEGNGQGMLOQDFANRFPVGGCVTSAGLVQEEIRFLINPELIVSRLFTEVLDH  
 Mparg 680 EKK....PTGLVTFIRQS..L..ED..F..PEWERCEKPL..TRLEVTTIEGNGQGMLOQDFANRFPVGGCVTGAGLVQEEIRFLINPELIVSRLFTEVLDH  
 Dparg 310 KRDASNVPTGVVTPVRRSGLPE..L..IDWSQSAAPLGDPVPLHVDAEKTIEDEGIGLLQVDFANKYLGGGVLGNGCVQEEIRFVICPELLVGKLFTECLRP  
 Ceparg 463 DKMSKDPDDGAVSF..RLTKMDKDTFNEEM..DKKLRSLPVEEFFDEMLIEDTAL..CTQVDFPAKEHGGVNLHEGSVQEEIRFLMCPEHHVGMLLCEKMKQ

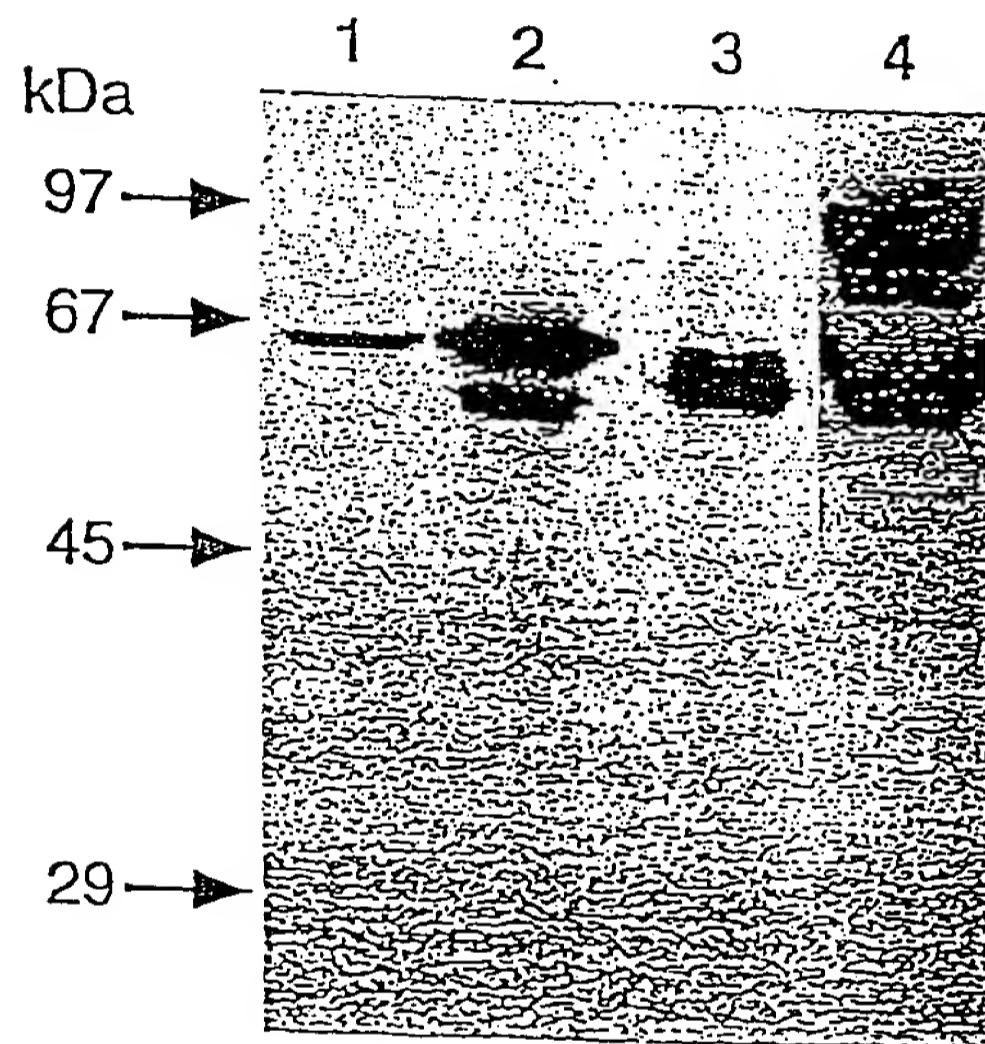
Bparg 779 HECLITITGTEQISSEITGIAETIRWA....RSEEDRSE..RDDMQRRTTIRVAIDALEFPR..RYLD....QFVPEKIRRELHKAYICGFLRPGVSESELSAVA  
 Bparg 778 HECLITITGTEQISSEITGIAETIRWA....RSEEDGSE..RDDCERRCTEIRVAIDALEFPR..RYLD....QFVPEKMRRELHKAYICGFLRPGVSESELSAVA  
 Mparg 770 HECLITITGTEQISSEITGIAETIRWA....RSEEDGSE..KDDMQRRTTIRVAIDALEFPR..RYLD....QFVPEKMRRELHKAYICGFLRPGVSESELSAVA  
 Dparg 408 FEALVMLGAERTISSEITGIAETIRWA....CNFDOSTP..RDSSGRRQTAIVVAIDALEFPR..QSHH....QIREDLKERRELHKAYICGFLRPGVSESELSAVA  
 Ceparg 560 LEAISIVGAIVFSEKETGIGTLEKNAELQPNESRQNTHEFRDRFGRRLRVETIAIDAILFEGSKLDQCTEQLNKAIIKEMKASIGFMSQGPXFTNIP..IV

Bparg 668 TGHWGGCAFGGDARLKALIQILAAVAERDVVIFTFGDSELMDIISMHTFLTERKLTVGR..VYKLLRLRYIHEECRNCSTPGP.....DIKLYPFIYHA  
 Bparg 867 TGHWGGCAFGGDARLKALIQILAAAERDVVIFTFGDSELMDIISMHTFLTERKLTVGR..VYKLLRLRYIHEECRNCSTPGP.....DIKLYPFIYHA  
 Mparg 859 TGHWGGCAFGGDARLKALIQILAAAERDVVIFTFGDSELMDIISMHTFLTERKLTVGR..VYKLLRLRYIHEECRNCSTPGP.....DIKLYPFIYHA  
 Dparg 495 TGHWGGCAFGGDSILKALLQLMVCAGLGRPLAYITFGNVEFRDDFHERWLLFRNDDITVQQ..LWS..ILRSYSLIKEKSSKEPREMKASKKELYDFI...  
 Ceparg 659 TGHWGGCAFNGDKPLKIIQVIAAGVADRPLHEFCBYGKPELAACKKIIERMKQKDVTLGKSCFSIFS-----

Bparg 961 VESCTQTTNQPGQRTGA-----  
 Bparg 960 VESCAETADHESGQRTGT-----  
 Mparg 952 VESSAETTDHMPGQKAGT-----  
 Dparg 590 KRELKKVRDVPGEGASAEAGSSRVAGLGEGRSETSAKSSPELMRQPARPQITITQQSTDLLPAQLSQDNNSSEDQALLMLSDDDEKANAHMEEASLEAKS  
 Ceparg 727 -----

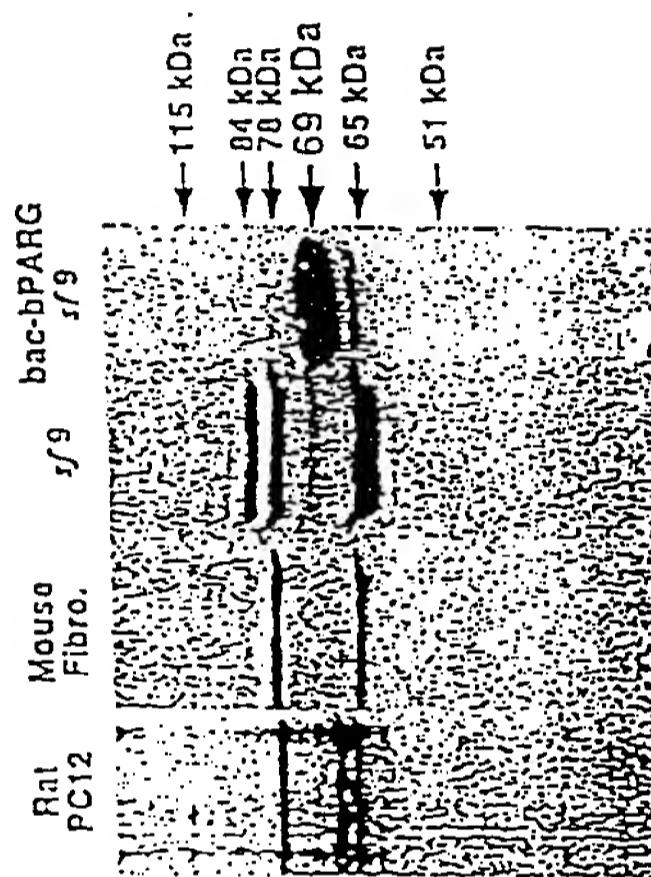
Bparg 978 -----  
 Bparg 977 -----  
 Mparg 969 -----  
 Dparg 690 SVEISMSSTTSKTSSTATKSMGSGGRQLSLLMLDTHYEGSASKRPRKSPHCSKAEGSAKSREIDVTDKDEKDDIVD  
 Ceparg 727 -----

FIGURE 17

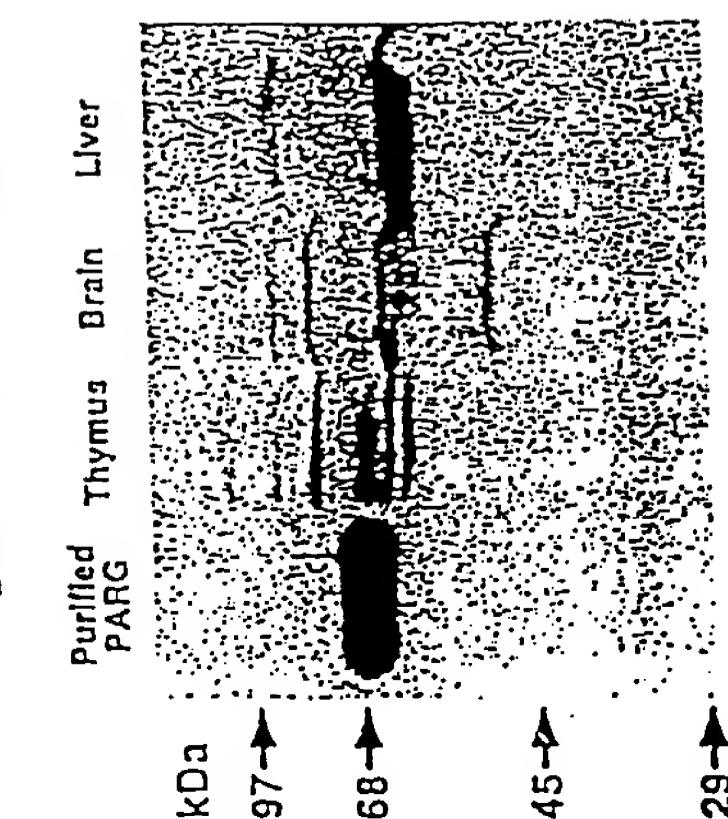


# FIGURE 18

## Cell Extracts



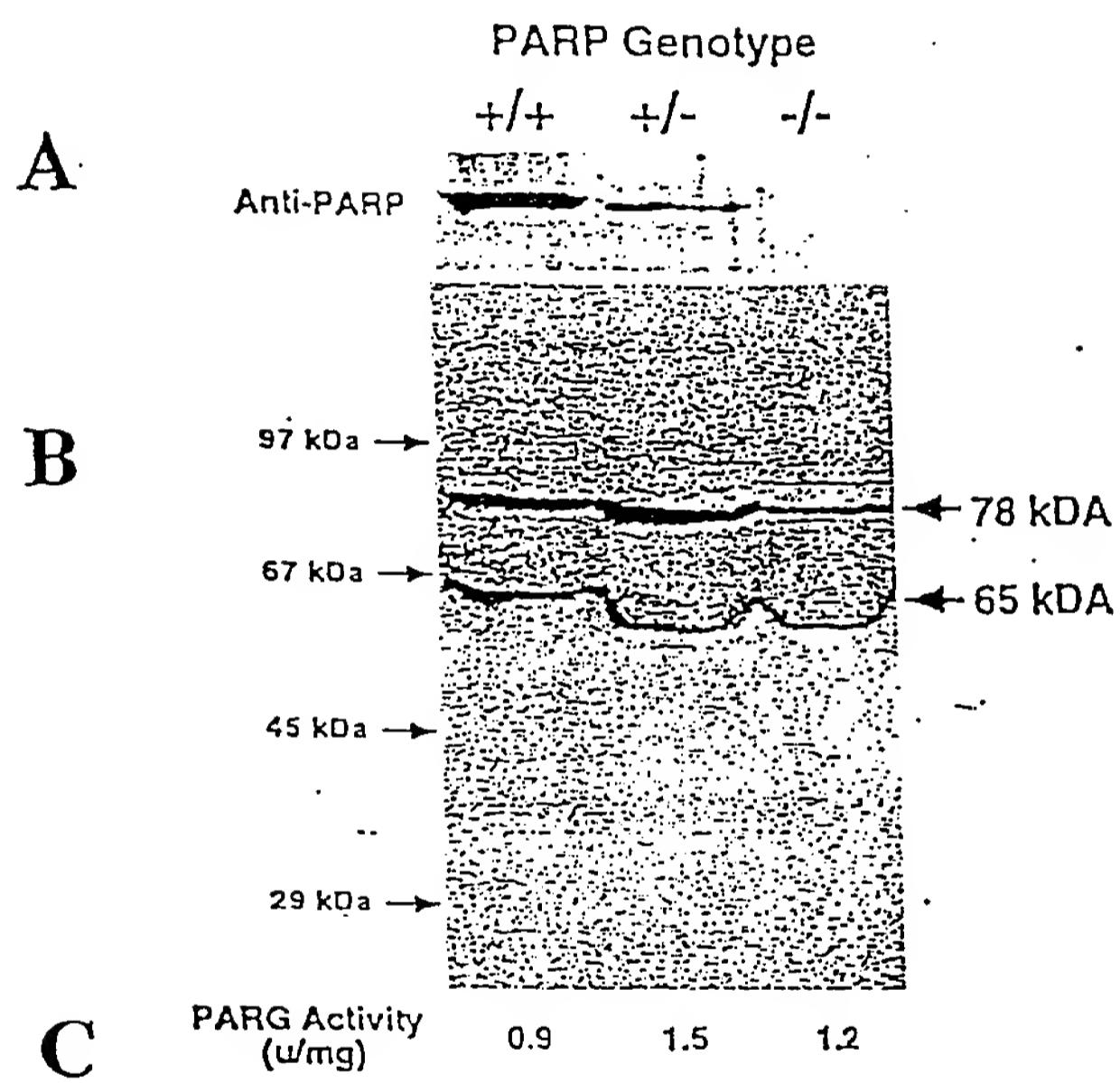
## Bovine Tissue



A

B

FIGURE 19



# FIGURE 20

Genomic cloning of the PARC gene

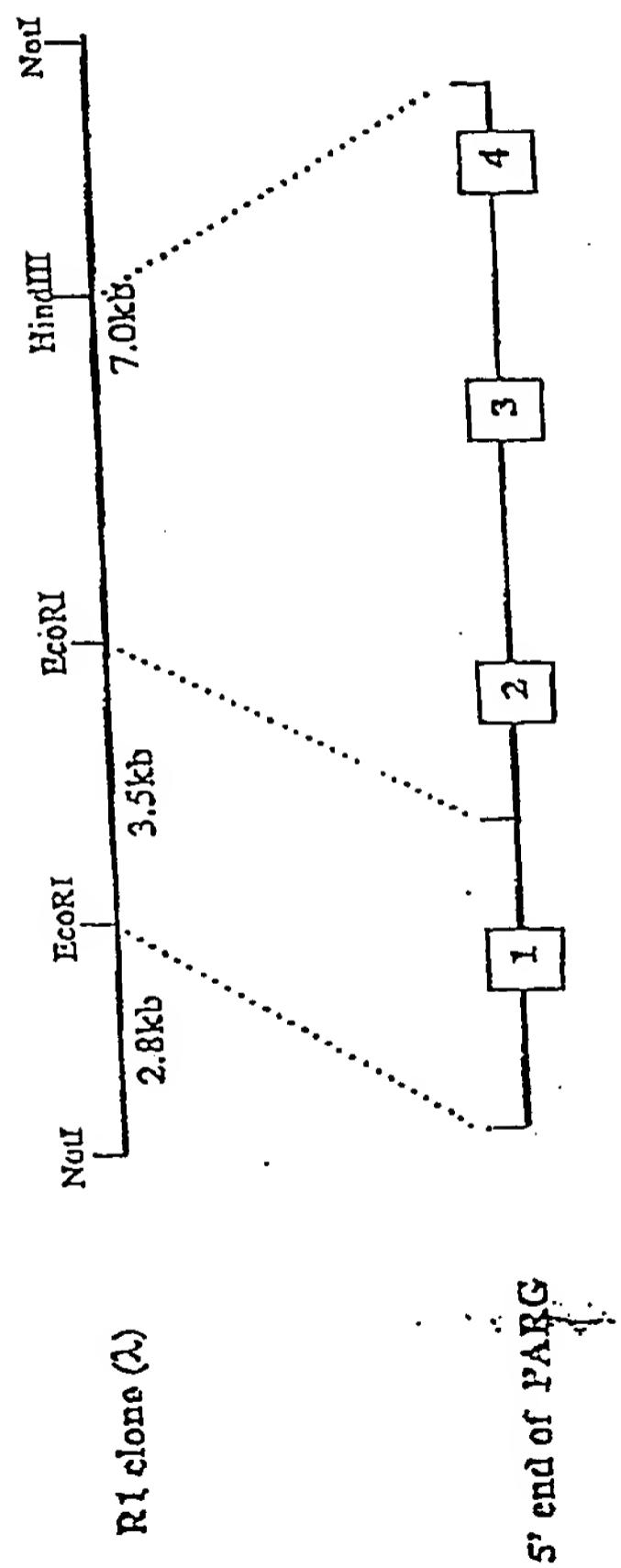


FIGURE 21.10 ES cell targeted PARG

